

Figure 1

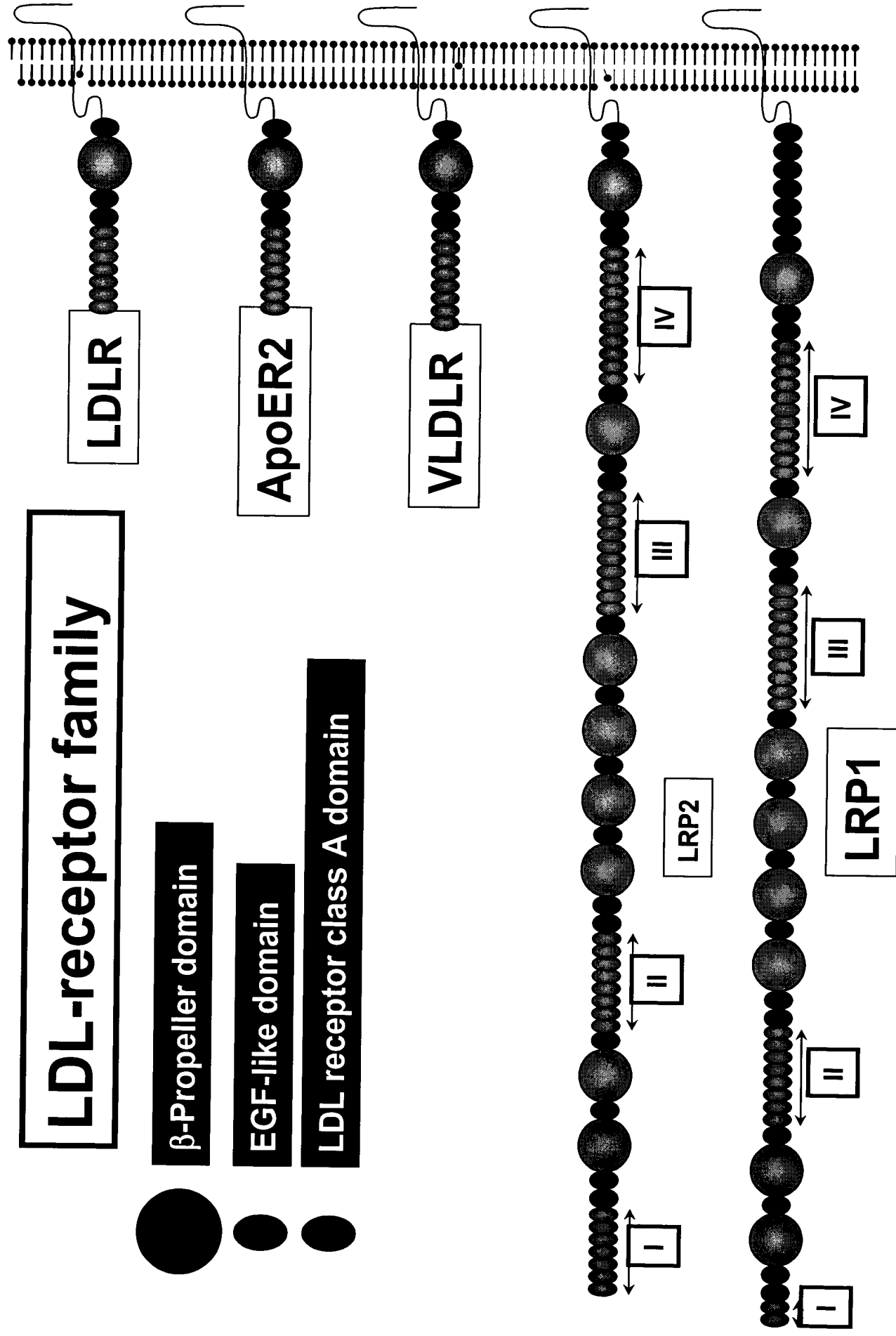


Figure 2

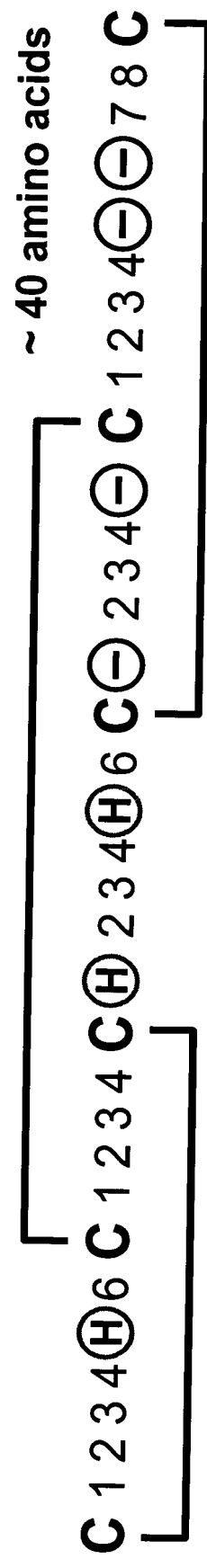
LDL-receptor class A domain

LRP1_HUMAN	C.EPYQFRCKNNR.....CVPGRWQ.CDYDNDCGDNSDEES.....C
LRP1_HUMAN	C.LPSQFKCTNTNR.....CIPGIFR.CNGQDNCGDGEDERD.....C
LDLR_HUMAN	C.SQDEFRCHDGK.....CISRQFV.CDSDRDCLDGSDEAS.....C
LRP2_HUMAN	C.SSSAFTCGHGE.....CIPAHWR.CDKRNDKVDGSDEHN.....C
LRP2_HUMAN	C.SSSEFQCASGR.....CIPQHWY.CDQETDCFDASDEPAS....C
CORI_HUMAN	CHSQGLVECRNGQ.....CIPSTFQ.CDGDEDCKDGSDEEN.....C
MAT_HUMAN	C.PAQTFRCSNGK.....CLSKSQQ.CNGKDDCGDGSDEAS.....C
CO8B_HUMAN	C...EGFVCAQTGR.....CVNRRLL.CNGDNDCGDQSDEAN.....C
MAT_HUMAN	C.TKHTYRCLNGL.....CLSKGNPECDGKEDCSDGSDEKD.....C
LDVR_HUMAN	CLGPGKFKCRSGE.....CIDISKV.CNQEQDCRDWSDEPLKE..C
APOER2_HUM	C.PAEKLSCGPTSHK...CVPASWR.CDGEKDCEGGADEAG.....C
SORL_HUMAN	CTHFMDFVCKNRQQ.....CLFHSMV.CDGIIQCRDGSDEDAAFAGC
ST7_HUMAN	C.AYNQFQCLSRFTKVYTCLPESLK.CDGNIDCLDLGDEID.....C
consensus	C.1234F6C12G4.....CI23456.CDG34DC1D3SDE78.....C

FIGURE 3

A-domains

A



B

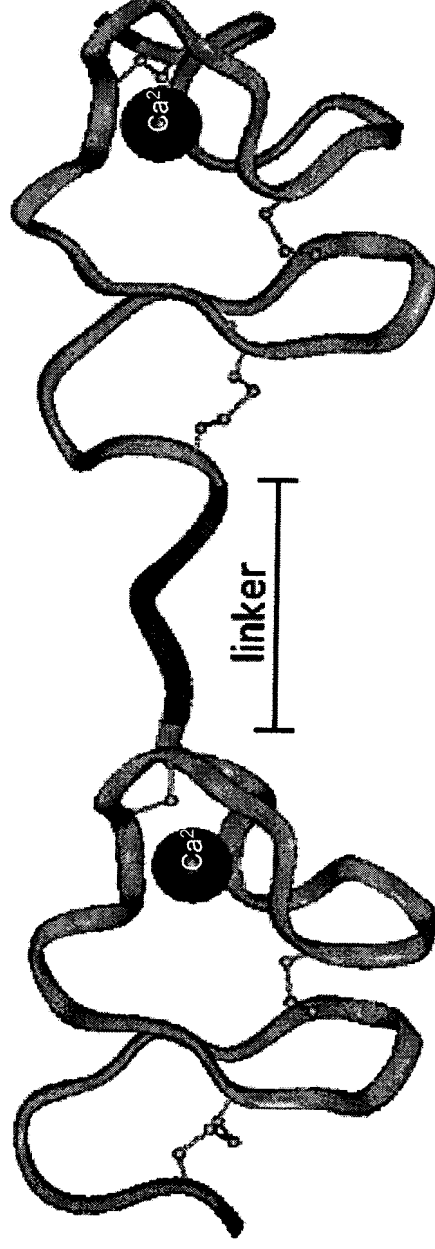


Figure 4

Ligands recognized by LDL-receptor family

<i>proteases</i>		<i>proteins involved in</i>	<i>miscellaneous</i>
factor IXa		<i>lipoprotein metabolism</i>	albumin
pro-uPA		apoB100	transthyretin
t-PA		apoE	β -Amyloid precursor protein
plasminogen		apoJ (clusterin)	RAP
MMP-9		apoH (β_2 -glycoprotein I)	complement C3
		Lp(a)	lactoferrin
<i>inhibitors</i>		hepatic lipase	thyroglobulin
α_2 -macroglobulin		lipoprotein lipase	thrombospondin
PAI-1		IDL	saposin precursor
TFPI		VLDL	reelin
pancreatic trypsin inhibitor		β -VLDL	insulin
			parathyroid hormone (PTH)
<i>complexes</i>			aprotinin
protease/		<i>non-human</i>	α -amylase
α_1 -antitrypsin		pseudomonas exotoxin A	C1q
protein C inhibitor		circumsporozoite protein	α_1 -microglobulin
protease nexin-1		trichosanthin	β_2 -microglobulin
antithrombin		ricin A	odorant-binding protein
C1-inhibitor		saporin	epidermal growth factor
thrombin/heparin cofactor II			prolactin
cathepsin G/ α_1 -antichymotrypsin		<i>antibiotics</i>	lysozyme
		gentamicin	connective tissue growth factor (CTGF)
		polymyxin B	cytochrome c
<i>vitamin-carrier complexes</i>		<i>viruses</i>	seminal vesicle secretory protein II
vitamin D-bp, vitamin D		HRV2 (Rhino)	clara cell secretory protein (CCSP)
retinol-bp, vitamin A		HCV (Flavi)	cubulin
transcobalamin, vitamin B12		BVDV (Flavi)	factor VIII

Figure 5

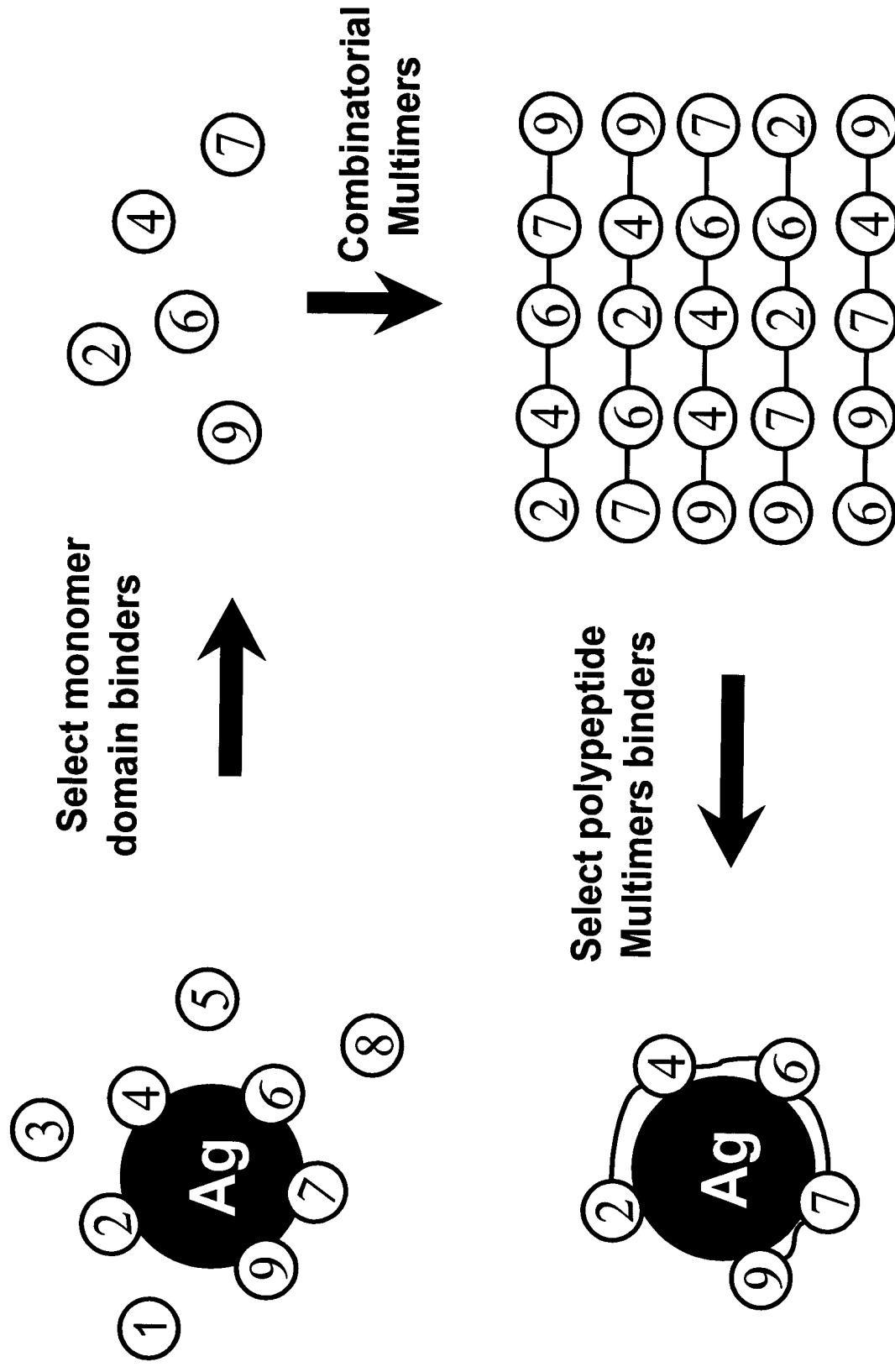


Figure 6

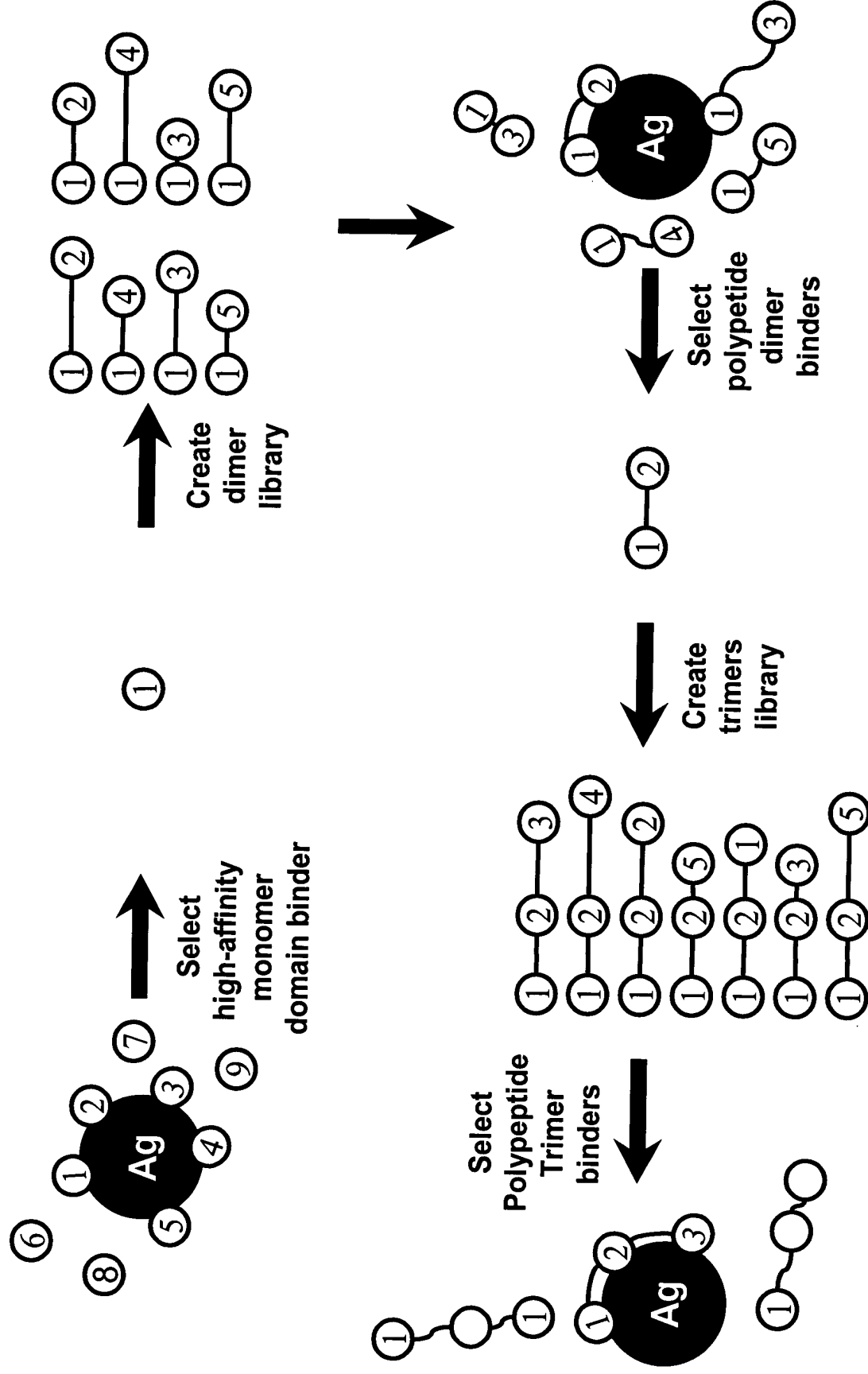


Figure 7

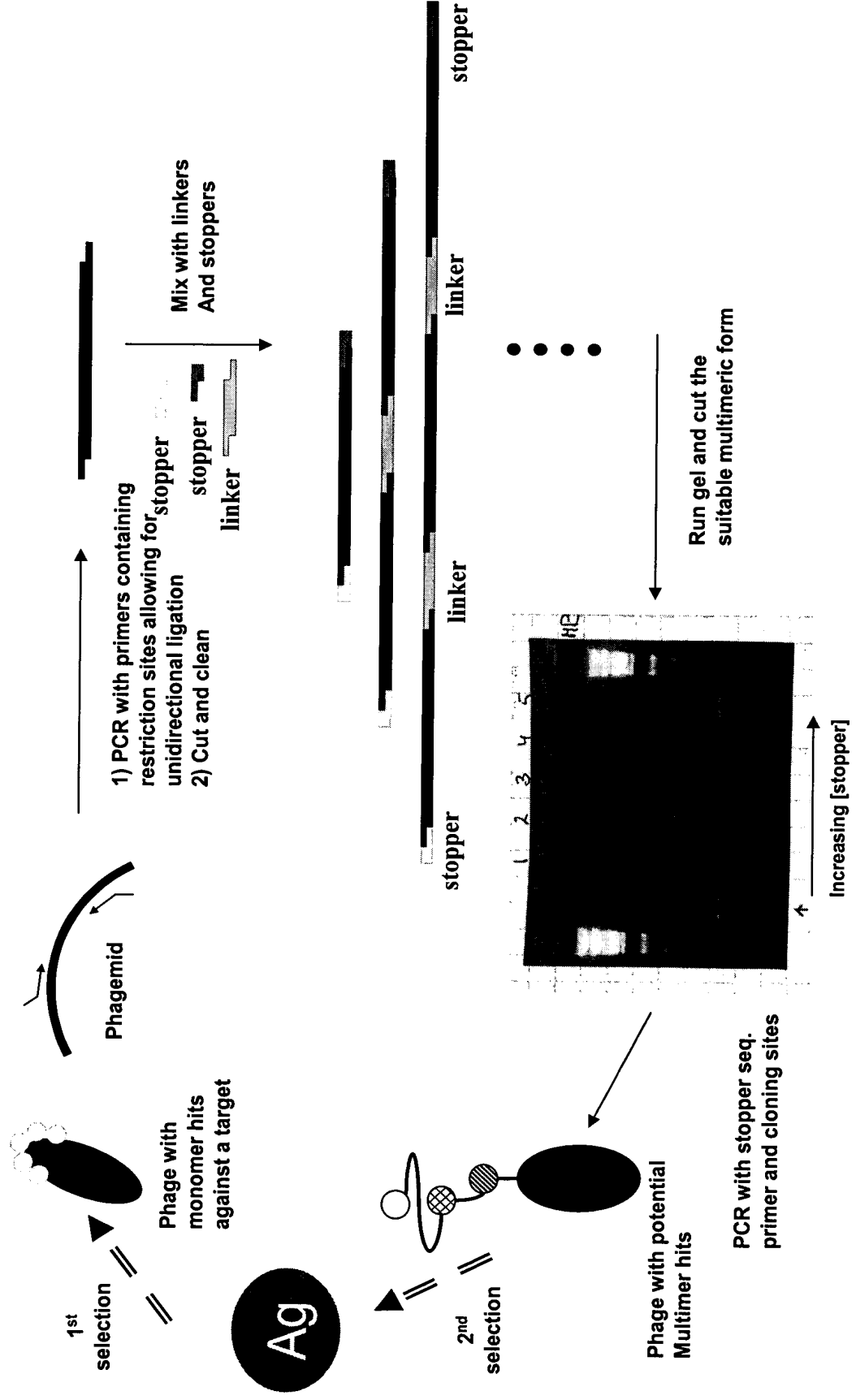


FIG. 9A

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
A	0.0	<u>7.1</u>	12.3	3.2	1.9	1.9	7.1	0.0	15.8	1.5	0.0	1.5	0.0	1.0	3.7	7.3	9.4
C	100.0	0.0	0.6	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	1.5	99.5	0.0	0.0	0.0	0.0
D	0.0	5.2	4.5	19.5	2.6	0.0	0.0	0.0	8.3	<u>10.5</u>	2.3	0.8	0.0	0.0	3.7	1.6	4.7
E	0.0	4.5	9.7	2.6	37.0	0.0	3.9	0.0	3.8	0.0	0.8	9.8	0.0	0.0	1.6	7.3	7.3
F	0.0	0.6	0.0	3.9	1.9	76.0	0.6	0.0	0.8	0.0	0.0	0.8	0.0	0.5	1.6	2.1	2.6
G	0.0	13.0	3.2	16.2	1.9	0.0	0.0	0.0	12.8	0.8	72.2	2.3	0.0	0.0	3.1	<u>5.2</u>	4.2
H	0.0	1.9	1.3	<u>5.2</u>	3.9	1.9	3.9	0.0	3.0	0.8	4.5	9.0	0.0	0.0	4.7	3.1	5.8
I	0.0	0.0	1.3	0.0	0.0	3.9	0.6	0.0	0.0	0.0	0.0	2.3	0.0	63.9	0.0	<u>5.2</u>	3.7
K	0.0	3.9	3.9	1.9	1.9	0.6	<u>7.8</u>	0.0	11.3	0.0	3.0	<u>9.0</u>	0.0	2.1	2.1	9.9	3.7
L	0.0	8.4	4.5	0.0	1.3	3.9	3.9	0.0	1.5	0.0	1.5	4.5	0.0	<u>11.0</u>	<u>5.2</u>	12.0	3.1
M	0.0	0.6	0.6	0.0	1.3	0.6	1.9	0.0	0.0	0.0	0.0	0.8	0.0	0.0	0.5	3.1	1.6
N	0.0	1.9	0.6	13.6	1.3	0.0	1.9	0.0	<u>5.3</u>	51.9	<u>5.3</u>	3.8	0.0	0.0	<u>5.2</u>	4.2	2.6
P	0.0	10.4	33.8	1.3	0.0	0.0	9.7	0.0	4.5	0.0	0.0	0.0	0.0	0.0	45.5	7.3	2.1
Q	0.0	10.4	2.6	1.9	30.5	0.6	21.4	0.0	5.3	0.8	2.3	9.8	0.0	0.0	2.6	5.8	4.7
R	0.0	7.1	3.2	3.2	1.3	0.6	18.2	0.0	<u>7.5</u>	0.8	4.5	32.3	0.0	0.0	1.0	<u>9.4</u>	11.5
S	0.0	18.8	11.7	16.2	3.9	0.6	9.7	0.0	15.0	25.6	3.0	3.0	0.0	0.0	14.7	10.5	20.4
T	0.0	<u>5.2</u>	2.6	<u>5.8</u>	3.2	1.3	<u>7.8</u>	0.0	2.3	<u>6.0</u>	0.8	<u>6.0</u>	0.0	1.6	2.6	0.5	<u>5.8</u>
V	0.0	0.6	1.9	0.6	0.0	0.6	1.3	0.0	2.3	0.8	0.0	3.0	0.0	<u>17.3</u>	0.5	3.1	2.6
W	0.0	0.0	0.6	1.9	0.0	1.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	2.6
Y	0.0	0.0	0.6	2.6	<u>5.8</u>	5.2	0.0	0.0	0.8	0.8	0.0	0.0	0.5	2.6	1.0	2.1	1.6
	100.0	85.7	67.5	76.6	73.4	81.2	81.8	100.0	81.2	94.0	77.4	75.9	99.5	92.1	70.7	80.1	60.2
	1	9	4	6	3	2	7	1	8	4	2	6	1	3	4	10	6
	100.0	73.4	67.5	65.6	67.5	76.0	66.2	100.0	68.4	77.4	72.2	60.9	99.5	63.9	60.2	60.2	59.2
	1	7	4	4	2	1	5	1	6	2	1	4	1	1	2	7	6

FIG. 9B

18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
1.6	2.6	0.0	0.0	1.0	2.5	<u>5.6</u>	0.0	0.0	<u>6.9</u>	0.0	4.6	4.6	0.0	0.0	16.0	3.8	0.0
0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
1.0	0.0	0.0	81.2	1.5	28.4	22.3	86.3	0.0	3.8	89.3	1.5	0.0	100.0	0.0	6.9	21.4	0.0
1.0	1.6	0.0	0.0	2.0	15.7	<u>4.6</u>	3.6	0.0	9.9	0.0	2.3	6.9	0.0	100.0	16.8	0.8	0.0
<u>7.9</u>	0.5	0.0	0.0	0.5	4.6	3.0	0.0	0.0	0.0	0.0	0.8	0.0	0.0	0.0	1.5	0.8	0.0
1.0	0.0	0.0	0.0	66.0	0.5	0.0	0.0	0.0	30.5	1.5	48.9	1.5	0.0	0.0	0.8	22.9	0.0
0.0	2.6	0.0	0.0	3.6	4.1	1.5	3.6	0.0	0.8	0.8	2.3	0.0	0.0	0.0	2.3	6.1	0.0
0.0	4.7	0.0	0.0	0.0	4.6	2.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	3.1	0.8	0.0
<u>6.8</u>	<u>12.6</u>	0.0	0.0	1.0	2.5	<u>5.1</u>	0.0	0.0	6.1	0.0	3.8	0.0	0.0	0.0	12.2	0.8	0.0
<u>14.7</u>	15.2	0.0	0.0	1.5	2.0	3.0	0.0	0.0	<u>6.9</u>	0.0	1.5	0.8	0.0	0.0	9.9	0.8	0.0
0.5	1.0	0.0	0.0	1.5	1.0	0.0	0.0	0.0	1.5	0.0	3.1	0.8	0.0	0.0	1.5	0.8	0.0
2.1	0.0	0.0	18.8	3.6	2.0	21.3	4.1	0.0	0.0	4.6	14.5	0.0	0.0	0.0	1.5	33.6	0.0
0.0	0.5	0.0	0.0	0.0	0.0	10.7	0.0	0.0	9.9	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.0
<u>5.8</u>	<u>7.3</u>	0.0	0.0	4.1	10.7	4.6	1.5	0.0	<u>5.3</u>	0.8	3.1	0.0	0.0	0.0	6.1	0.8	0.0
3.7	24.1	0.0	0.0	5.6	2.5	6.1	0.0	0.0	3.8	0.0	2.3	3.1	0.0	0.0	<u>10.7</u>	1.5	0.0
1.0	0.0	0.0	0.0	3.0	2.0	2.0	0.5	0.0	7.6	1.5	4.6	80.9	0.0	0.0	0.8	4.6	0.0
0.5	2.6	0.0	0.0	2.5	1.5	2.0	0.5	0.0	0.8	0.8	0.0	1.5	0.0	0.0	2.3	0.0	0.0
1.0	21.5	0.0	0.0	0.5	10.2	3.6	0.0	0.0	4.6	0.0	0.0	0.0	0.0	0.0	<u>6.1</u>	0.0	0.0
46.6	2.6	0.0	0.0	0.5	2.0	1.5	0.0	0.0	0.0	0.0	3.1	0.0	0.0	0.0	0.8	0.0	0.0
4.7	0.5	0.0	0.0	1.5	3.0	1.0	0.0	0.0	0.0	0.8	3.8	0.0	0.0	0.0	0.8	0.0	0.0
81.7	80.6	100.0	100.0	71.6	65.0	71.1	86.3	100.0	83.2	89.3	63.4	87.8	100.0	100.0	84.7	84.0	100.0
5	5	1	2	2	4	6	1	1	8	1	2	2	1	1	8	4	1
61.3	60.7	100.0	81.2	66.0	65.0	60.4	86.3	100.0	64.1	89.3	63.4	80.9	100.0	100.0	61.1	77.9	100.0
2	3	1	1	1	4	4	1	1	5	1	2	1	1	1	5	3	1

Figure 10

	a	b c	de	f ghi	jk lm	nop	q
IDD_HUMAN	C.....	NPGQFACRSGTIQ.....	CIPLPWQ.CDGWATCEDE.....	SDEAN.....	C		
LRP3_HUMAN	C.....	QADEFRCDNGK.....	CLPGPWQ.CNTVDECGDG.....	SDEGN.....	C		
LRP3_HUMAN	C.....	PGGTFFPCSGARSTR.....	CLPVERR.CDGLQDCGDG.....	SDEAG.....	C		
LRP3_HUMAN	C.....	LPWEQPCGSSSDSDGSLGDQGC	CFSEPQR.CDGWWHCASG.....	RDEQG.....	C		
LRP3_HUMAN	C.....	PPDQYPCEGGSSGL.....	CYTPADR.CNNQKSCPDG.....	ADEKN.....	C		
LRP3_HUMAN	C.....	QPGTFHCGTNL.....	CIFETWR.CDGQEDCQDG.....	SDEHG.....	C		
LRP5_HUMAN	C.....	SPDQFACATGEID.....	CIPGAWR.CDGFPEDDDQ.....	SDEEG.....	C		
LRP5_HUMAN	C.....	SAAQFPCARGQ.....	CVDLRLR.CDGEADCQDR.....	SDEVD.....	C		
LRP5_HUMAN	C.....	LPNQFRCASGQ.....	CVLIKQQ.CDSFPDCIDG.....	SDELM.....	C		
LRP6_HUMAN	C.....	SPQQFTCFTGEID.....	CIPVAWR.CDGFTCEDH.....	SDELN.....	C		
LRP6_HUMAN	C.....	SESQFQCASGQ.....	CIDGALR.CNGDANCQDK.....	SDEKN.....	C		
LRP6_HUMAN	C.....	LIDQFRCANGQ.....	CIGKHKK.CDHNVDCCSDK.....	SDELD.....	C		
ST7_HUMAN	C.....	ACDQFRCGNGK.....	CIPPAWK.CNNMDECGDS.....	SDEEI.....	C		
ST7_HUMAN	C.....	AYNQFQCLSRFTKVYT.....	CLPESLK.CDGNIDCLDL.....	GDEID.....	C		
ST7_HUMAN	C.....	LPWEIPCGGNWG.....	CYTEQQR.CDGYWHCPNG.....	RDETN.....	C		
ST7_HUMAN	C.....	QKEEFPCSRNGV.....	CYPRSDR.CNYQNHCPNG.....	SDEKN.....	C		
ST7_HUMAN	C.....	QPGNFHCKNNR.....	CVFESWV.CDSQDDCGDG.....	SDEEN.....	C		
CORI_HUMAN	C.....	GRGENFLCASGI.....	CIPGKLQ.CNGYNDCCDW.....	SDEAH.....	C		
CORI_HUMAN	C.....	SENLFHCHTGK.....	CLNYSLV.CDGYDDCGDL.....	SDEQN.....	C		
CORI_HUMAN	C.....	NPTTEHRCGDGR.....	CIAMEWV.CDGDHDCVDK.....	SDEVN.....	C		
CORI_HUMAN	C.....	HSQGLVECRNGQ.....	CIPSTFQ.CDGEDDCKDG.....	SDEEN.....	C		
CORI_HUMAN	C.....	SPSHFKCRSGQ.....	CVLASRR.CDGQADCCDD.....	SDEEN.....	C		
CORI_HUMAN	C.....	KERDLWECPSNKQ.....	CLKHTVI.CDGFDPDPCDY.....	MDEKN.....	C		
CORI_HUMAN	C.....	QDDELECANHA.....	CVSRDLW.CDGEADCCSDS.....	SDEWD.....	C		
TMS2_HUMAN	C.....	SNSGIECDSSGT.....	CINPSNW.CDGVSHCPGG.....	EDENR.....	C		
TMS3_HUMAN	C.....	SGKYRCRSSFK.....	CIELIAR.CDGVSDCKDG.....	EDEYR.....	C		
MAT_HUMAN	C.....	PGQFTCRTGR.....	CIRKELR.CDGWADCTDH.....	SDELN.....	C		
MAT_HUMAN	C.....	DAGHQFTCKNKF.....	CKPLFWV.CDSVNDCCGN.....	SDEQG.....	C		
MAT_HUMAN	C.....	PAQTFRCNSGK.....	CLSKSQQ.CNGKDDCGDG.....	SDEAS.....	C		
MAT_HUMAN	C.....	TKHTYRCLNGL.....	CLSKGNPECCKEDCCSDG.....	SDEKD.....	C		
ENTK_HUMAN	C.....	LPGSSPCTDALT.....	CIKADLF.CDGEVNCPCDG.....	SDEDNKM.....	C		
ENTK_HUMAN	C.....	KADHFQCKNGE.....	CVPLVNL.CDGHLCEDG.....	SDEAD.....	C		
HAI1_HUMAN	C.....	QPTQFRCNSGC.....	CIDSFLE.CDDTPNCPDA.....	SDEAA.....	C		
CFAI_HUMAN	C.....	YTQKADSPMDFFQCVNGK.....	YISQMKK.CDGINDCGDQ.....	SDEL.....	C		
CFAI_HUMAN	C.....	QKGKFHCKSGV.....	CIPSQYQ.CNGEVDCITG.....	EDEVG.....	C		
CO6_HUMAN	C.....	KNKFRCDSGR.....	CIARKLE.CNGENDCCGN.....	SDERD.....	C		
CO7_HUMAN	C.....	GERFRCFSGQ.....	CISKSLV.CNGDSDCCDEDS.....	ADEDR.....	C		
CO8A_HUMAN	C.....	GQDFQCKETGR.....	CLKRHLV.CNGDQDCLDG.....	SDEDD.....	C		
CO8B_HUMAN	C.....	EGFVCAQTGR.....	CVNRRLL.CNGDNDCCGDQ.....	SDEAN.....	C		
CO9_HUMAN	C.....	GNDFQCSTGR.....	CIKMRLR.CNGDNDCCGDF.....	SDEDD.....	C		
PERL_HUMAN	C.....	TEAEFACHSYNE.....	CVALEYR.CDRRPDCRDM.....	SDELN.....	C		
PERL_HUMAN	C.....	GPQEAACRNHG.....	CIPRDYL.CDGQEDCEDG.....	SDELD.....	C		
PERL_HUMAN	C.....	EPNEFFPCGNHG.....	CALKLWR.CDGFDFCEDR.....	TDEAN.....	C		
PERL_HUMAN	C.....	GPTQFRCVSTNM.....	CIPASFH.CDEESDCPDR.....	SDEFG.....	C		
SORL_HUMAN	C.....	LRNQYRCNSGN.....	CINSIWW.CDFDNDCCGDM.....	SDERN.....	C		
SORL_HUMAN	C.....	DLDTQFRCQESGT.....	CIPLSYK.CDLEDDCCGN.....	SDESH.....	C		
SORL_HUMAN	C.....	RSDEYNCCSGM.....	CIRSSWV.CDGDNDCCRDW.....	SDEAN.....	C		
SORL_HUMAN	C.....	EASNFOCRNGH.....	CIPQRAW.CDGDTCQDG.....	SDEDPVN.....	C		
SORL_HUMAN	C.....	NGFRCPNGT.....	CIPSSKH.CDGLRDCSDG.....	SDEQH.....	C		
SORL_HUMAN	C.....	THFMDFVCKNRQQ.....	CLFHSMV.CDGIIQCRDG.....	SDEDAAFAG.....	C		
SORL_HUMAN	C.....	DEFGFQCQNGV.....	CISLIWK.CDGMDDCCGDY.....	SDEAN.....	C		
SORL_HUMAN	C.....	SRYFQFRCENGH.....	CIPNRWK.CDRENDCCGDW.....	SDEKD.....	C		
SORL_HUMAN	C.....	LPNYRCSSGT.....	CVMDTWV.CDGYRDCADG.....	SDEEA.....	C		
SORL_HUMAN	C.....	DRFEFECHQPKT.....	CIPNWKR.CDGHQDCQDG.....	RDEAN.....	C		
SORL_HUMAN	C.....	MSREFQCEDGEA.....	CIVLSEK.CDGFLDCSDE.....	SDEKA.....	C		
APOER2_HUM	C.....	EKDQFQCRNER.....	CIPSVWR.CDEDDDCLDH.....	SDEDD.....	C		
APOER2_HUM	C.....	ADSDFTCDNGH.....	CIHERWK.CDGEEDCPDG.....	SDESEAT.....	C		
APOER2_HUM	C.....	PAEKLSCGPTSHK.....	CVPASWR.CDGEKDCGG.....	ADEAG.....	C		
APOER2_HUM	C.....	APHEFQCGNRS.....	CLAAVVF.CDGDDDCGDG.....	SDEAG.....	C		
APOER2_HUM	C.....	GPREFRCGGDGGGA.....	CIPERWV.CDRQFDCEDR.....	SDEAAEL.....	C		
APOER2_HUM	C.....	ATVSQFACRSGE.....	CVHLGWR.CDGDRCCKDK.....	SDEAD.....	C		
APOER2_HUM	C.....	RGDEFQCGDGT.....	CVLAIKH.CNQEQDCPDG.....	SDEAG.....	C		
LDLR_HUMAN	C.....	ERNEFQCCQDGK.....	CISYKWW.CDGSACQDG.....	SDESQET.....	C		
LDLR_HUMAN	C.....	KSGDFSCGGRVNR.....	CIPQFWR.CDGQVDCDNG.....	SDEQG.....	C		
LDLR_HUMAN	C.....	SQDEFRCCHDGK.....	CISRQFV.CDSDRDCLDG.....	SDEAS.....	C		
LDLR_HUMAN	C.....	GPASFQCNST.....	CIPQLWA.CDNDPDCEDG.....	SDEWPQR.....	C		
LDLR_HUMAN	C.....	SAFEFHCLSGE.....	CIHSSWR.CDGGPDCKDK.....	SDEEN.....	C		
LDLR_HUMAN	C.....	RPDEFQCSGDN.....	CIHGSRQ.CDREYDCKDM.....	SDEVG.....	C		
LDLR_HUMAN	C.....	EGPNKFKCHSGE.....	CITLDKV.CNMARDCCRDW.....	SDEPIKE.....	C		
LDVR_HUMAN	C.....	EPSQFQCTNGR.....	CITLLWK.CDGEDDCVDG.....	SDEKN.....	C		
LDVR_HUMAN	C.....	AESDFVCNNGQ.....	CVPSRWK.CDGDPCEDG.....	SDESPQ.....	C		

LDVR_HUMAN	C.....RIHEISCGAHSTQ.....CIPVSWR.CDGENDCDSG.....EDEEN.....C
LDVR_HUMAN	C.....SPDEFTCSSGR.....CISRNFW.CNGQDDCSDG.....SDELD.....C
LDVR_HUMAN	C.....GAHEFQCTSS.....CIPISWV.CDDADDCSDQ.....SDESLEQ.....C
LDVR_HUMAN	C.....PASEIQCGSGE.....CIHKKWR.CDGDPCCKDG.....SDEVN.....C
LDVR_HUMAN	C.....RPDQFECEDGS.....CIHGSRQ.CNGIRDCVDG.....SDEVN.....C
LDVR_HUMAN	C.....LGPGKFCKRSGE.....CIDISKV.CNQEQDCRDW.....SDEPLKE.....C
LRP1_HUMAN	C.....SPKQFACRDQIT.....CISKGWR.CDGERDCPDG.....SDEAPEI.....C
LRP1_HUMAN	C.....QPNEHNCGLTEL.....CVPMSRL.CNGVQDCMDG.....SDEGPH.....C
LRP1_HUMAN	C.....QPGEFACANSR.....CIQERWK.CDGDNDCLDN.....SDEAPAL.....C
LRP1_HUMAN	C.....PSDRFKCENNR.....CIPNRWL.CDGDNDCGNS.....EDESAT.....C
LRP1_HUMAN	C.....PPNQFSCASGR.....CIPISWT.CDLDDDCGDR.....SDESAS.....C
LRP1_HUMAN	C.....FPLTQFTCNNGR.....CININWR.CDNDNDCGDN.....SDEAG.....C
LRP1_HUMAN	C.....SSTQFKCNSGR.....CIPEHWT.CDGDNDCGDY.....SDETHAN.....C
LRP1_HUMAN	C.....HTDEFQCRDLGL.....CIPLRWR.CDGDTCMDG.....SDEKS.....C
LRP1_HUMAN	C.....DPSVKFGCKDSAR.....CISKAWV.CDGDNDCEDN.....SDEEN.....C
LRP1_HUMAN	C.....RPPSHPCANNTSV.....CLPPDKL.CDGDNDCGDG.....SDEGEL.....C
LRP1_HUMAN	C.....RAQDEFECANGE.....CINFSLT.CDGVPHCKDK.....SDEKPSY.....C
LRP1_HUMAN	C.....KKTFRCNSGR.....CVSNMLW.CNGADDCGDG.....SDEIP.....C
LRP1_HUMAN	C.....GVGEFRCRDGT.....CIGNSSR.CNQFVDCEDA.....SDEMNI.....C
LRP1_HUMAN	CSSYFRLGVKGVLFQPCERTSL.....CYAPSWV.CDGANDCGDY.....SDEER.....C
LRP1_HUMAN	C.....PLNYFACPSGR.....CIPMSWT.CDKEDDCHEG.....SDETH.....C
LRP1_HUMAN	C.....SEAQFECQNRH.....CISKQWL.CDGSDDCGDG.....SDEAAH.....C
LRP1_HUMAN	C.....GPSSFSCPGTHV.....CVPERWL.CDGDKDCADG.....ADESIAAG.....C
LRP1_HUMAN	C.....DDREFMCQNRQ.....CIPKHFV.CDHDRDCADG.....SDESPE.....C
LRP1_HUMAN	C.....GPSEFRCANR.....CLSSRQWECDEGNDCHDQ.....SDEAPKNPH.....C
LRP1_HUMAN	C.....NASSQFLCSSGR.....CVAEALL.CNGQDDCGDS.....SDERG.....C
LRP1_HUMAN	C.....TASQFVCKNDK.....CIPFWWK.CDTEDDCGDH.....SDEPPD.....C
LRP1_HUMAN	C.....RPGQFQCSGTI.....CTNPAFI.CDGDNDCCDN.....SDEAN.....C
LRP1_HUMAN	C.....LPSQFKCTNTNR.....CIPGIFR.CNGQDNCGDG.....SDEER.....C
LRP1_HUMAN	C.....APNQFQCSITKR.....CIPRVWV.CDRDNDCCVDG.....SDEPAN.....C
LRP1_HUMAN	C.....GVDEFRCCKDSGR.....CIPARWK.CDGEDDCGDG.....SDEPKEE.....C
LRP1_HUMAN	C.....EPYQFRCKNNR.....CVPGRWQ.CDYDNDCCDN.....SDEES.....C
LRP1_HUMAN	C.....SESEFSCANGR.....CIAGRWK.CDGDHDCADG.....SDEKD.....C
LRP1_HUMAN	C.....DMDQFQCKSGH.....CIPLRWR.CDADADCMDG.....SDEEA.....C
LRP1_HUMAN	C.....PLDEFQCNNTL.....CKPLAWK.CDGEDDCGDN.....SDENPEE.....C
LRP1_HUMAN	C.....PPNRPFRCCKNDRV.....CLWIGRQ.CDGTDCNGDG.....TDEED.....C
LRP1_HUMAN	C.....KDKKEFLCRNQR.....CLSSSLR.CNMFDCCGDG.....SDEED.....C
LRP2_HUMAN	C.....DSAHFRCGSGH.....CIPADWR.CDGTKDCSDD.....ADEIG.....C
LRP2_HUMAN	C.....QQGYFKCQSEGO.....CIPSSWV.CDQDQDCDDG.....SDEKQD.....C
LRP2_HUMAN	C.....SSHQITCSNGQ.....CIPSEYR.CDHVRDCPDG.....ADEND.....C
LRP2_HUMAN	C.....EQLTCDNGA.....CYNTSQK.CDWKVDCCDS.....SDEIN.....C
LRP2_HUMAN	C.....LHNEFSCNGE.....CIPRAYV.CDHNDCCQDG.....SDEHA.....C
LRP2_HUMAN	C.....GGYQFTCPSGR.....CIYQNWV.CDGEDDCKDN.....GDEEG.....C
LRP2_HUMAN	C.....SPREWSCPESGR.....CISYKIV.CDGILDCPGR.....EDENNTSTGKYC.....C
LRP2_HUMAN	C.....GLFSFPCKNGR.....CVPNYYL.CDGVDDCHDN.....SDEQL.....C
LRP2_HUMAN	C.....SSSAFTCGHGE.....CIPAHWR.CDKRNDCCVDG.....SDEHN.....C
LRP2_HUMAN	C.....LDTQYTCDNHQ.....CISKNWV.CDTDNDCCGDG.....SDEKN.....C
LRP2_HUMAN	C.....QPSQFNCPNHR.....CIDLSFV.CDGDKDCVDG.....SDEVG.....C
LRP2_HUMAN	C.....TASQFKCASGDK.....CIGVTNR.CDGVFDCSDN.....SDEAG.....C
LRP2_HUMAN	C.....HSDEFQCEQDGI.....CIPNFWC.CDGHPCCLYG.....SDEHNA.....C
LRP2_HUMAN	C.....PSSYFHCDNGN.....CIHRAWL.CDRDNDCCGDM.....SDEKD.....C
LRP2_HUMAN	C.....PSWQWQCLGHNI.....CVNLSVV.CDGIFDCPNG.....TDESPL.....C
LRP2_HUMAN	C.....GASSFTCSNGR.....CISEEWK.CDNDNDCCGDG.....SDEMSV.....C
LRP2_HUMAN	C.....SPTAFTCANGR.....CVQYSYR.CDYNDCCGDG.....SDEAG.....C
LRP2_HUMAN	C.....NATTEFCMNNRR.....CIPREFI.CNGVDNCHDNT.....SDEKN.....C
LRP2_HUMAN	C.....QSGYTKCHNSNI.....CIPRVYL.CDGDNDCCGDN.....SDENPTY.....C
LRP2_HUMAN	C.....SSSEFQASGR.....CIPQHWY.CDQETDCFDA.....SDEPAS.....C
LRP2_HUMAN	C.....LADEFKCDGGR.....CIPSEWI.CDGDNDCCGDM.....SDEDKRHQ.....C
LRP2_HUMAN	C.....SDSEFLCVNDRPPDRR.....CIPQSWV.CDGDVDCDGT.....YDENQN.....C
LRP2_HUMAN	C.....SENEFTCGYGL.....CIPKIFR.CDRHNDCCDY.....SDEGR.....C
LRP2_HUMAN	C.....QQNQFTCQNGR.....CISKTFV.CDEDNCCGDG.....SDELMHL.....C
LRP2_HUMAN	C.....PPHEFKCDNGR.....CIEMMKL.CNHLDDCLDN.....SDEKG.....C
LRP2_HUMAN	C.....SSTQFLCANNEK.....CIPWVKL.CDGQKDCSDG.....SDEAL.....C
LRP2_HUMAN	C.....RLGQFQCSGDN.....CTSPQTL.CNAHQNCPDG.....SDEDRLL.....C
LRP2_HUMAN	C.....DSNEWQCANKR.....CIPESWQ.CDTFNDCCDN.....SDESSH.....C
LRP2_HUMAN	C.....RPGQFRCANGR.....CIPQAWK.CDVNDCCGDH.....SDEPIEE.....C
LRP2_HUMAN	C.....DNFTEFSCKTNYR.....CIPKWAY.CNGVDDCRDN.....SDEQG.....C
LRP2_HUMAN	C.....HPVGDFRCKNHH.....CIPLRWQ.CDQNDCCGDN.....SDEEN.....C
LRP2_HUMAN	C.....TESEFRCVNQQ.....CIPSRWI.CDHYNDCCDN.....SDEER.....C
LRP2_HUMAN	C.....HPEYFQCTSGH.....CVHSELK.CDGSADCLDA.....SDEAD.....C
LRP2_HUMAN	C.....QATMFECKNHV.....CIPPYWK.CDGDCCCGDG.....SDEELHL.....C
LRP2_HUMAN	C.....NSPNRFRCDNNR.....CIYSHEV.CNGVDDCCGDG.....TDETEH.....C
LRP2_HUMAN	C.....TEYFYKCGNGH.....CIPHDNV.CDDADCCGDW.....SDELG.....C
LR1B_HUMAN	C.....DPGEFLCHDHVT.....CVSQSWL.CDGDPCPDG.....SDESLDT.....C
LR1B_HUMAN	C.....PLNHIACLGTNK.....CVHLSQL.CNGVLDCCPDG.....YDEGVH.....C
LR1B_HUMAN	C.....KAGEFRCKNRH.....CIQARWK.CDGDCCCLDG.....SDEDSVN.....C

LR1B_HUMAN	CPDDQFKCQNNR.....	CIPKRWL.CDGANDCGSN.....	EDESNOT.....	C	
LR1B_HUMAN	CQVDQFSCGNGR.....	CIPRAWL.CDREDDCGDQ.....	TDEMAS.....	C	
LR1B_HUMAN	CEPLTQFVCKSGR.....	CISSKWH.CDSDDDCGDG.....	SDEVG.....	C	
LR1B_HUMAN	CFDNQFRCSGR.....	CIPGHWL.CDGDNDGDF.....	SDEAQIN.....	C	
LR1B_HUMAN	CNGNEFQCHPDGN.....	CVPDWLR.CDGEKDCEDG.....	SDEKG.....	C	
LR1B_HUMAN	CDHKTKFSCWSTGR.....	CINKAWV.CDGDIDCEDQ.....	SDEDD.....	C	
LR1B_HUMAN	CGPPKHPCANDTSV.....	CLQPEKL.CNGKKDCPDG.....	SDEGYL.....	C	
LR1B_HUMAN	CNAYSEFECNGE.....	CIDYQLT.CDGI PHCKDK.....	SDEKLLY.....	C	
LR1B_HUMAN	CRRGFKPCYNRR.....	CIPHGKL.CDGENDCGDN.....	SDELD.....	C	
LR1B_HUMAN	CATVEFRCADGT.....	CIPRSAR.CNQNICADA.....	SDEKN.....	C	
LR1B_HUMAN	C	CTHFYKLGVKTTGFIRCNSTSL.....	CVLPTWI.CDGSNDGCDY.....	SDELK.....	C	
LR1B_HUMAN	CEENYFSCPSGR.....	CILNTWI.CDGQKDCEDG.....	RDEFH.....	C	
LR1B_HUMAN	CSWNQFACSAQK.....	CISKHWI.CDGEDDCGDG.....	LDESDSI.....	C	
LR1B_HUMAN	CAADMFSCQGSRA.....	CVPRHWL.CDGERDCPDG.....	SDELSTAG.....	C	
LR1B_HUMAN	CDENAFMCHNKV.....	CIPKQFV.CDHDDDCGDG.....	SDESPQ.....	C	
LR1B_HUMAN	CGTEEFSCADGR.....	CLLNTQWQCDGDFDCPDH.....	SDEAPLNPK.....	C	
LR1B_HUMAN	CNSSFFMCKNGR.....	CIPSGGL.CDNKDDCGDG.....	SDERN.....	C	
LR1B_HUMAN	CTASQFRCKTDK.....	CIPFWWK.CDTVDDCGDG.....	SDEPDD.....	C	
LR1B_HUMAN	CQPGRFQCGTGL.....	CALPAFI.CDGENDCGDN.....	SDELN.....	C	
LR1B_HUMAN	CLSGQFKCTKNQK.....	CIPVNLN.CNGQDDCGDE.....	EDERD.....	C	
LR1B_HUMAN	CSPDYFQCKTTKH.....	CISKLWV.CDEDPCADA.....	SDEAN.....	C	
LR1B_HUMAN	CGPHEFQCKNNN.....	CIPDHRW.CDSQNDCCSDN.....	SDEEN.....	C	
LR1B_HUMAN	CTLKDFLCANGD.....	CVSSRFW.CDGDFFCADG.....	SDERN.....	C	
LR1B_HUMAN	CSKDQFRCSNGQ.....	CIPAKWK.CDGHEDCYK.....	EDEKS.....	C	
LR1B_HUMAN	CSSREYICASDG.....	CISASLK.CNGEYDCADG.....	SDEMD.....	C	
LR1B_HUMAN	CKEDQFRCKNAH.....	CIPIRWL.CDGIHDCVDG.....	SDEEN.....	C	
LR1B_HUMAN	CRADEFLCNNSL.....	CKLHFWV.CDGEDDCGDN.....	SDEAPDM.....	C	
LR1B_HUMAN	CPSTRPHRCRNNRI.....	CLQSEQM.CNGIDECGDN.....	SDEDH.....	C	
LR1B_HUMAN	CKKDEFACSNKK.....	CIPMDLQ.CDRLDDCGDG.....	SDEQG.....	C	
075851	CAEGEALCQENGH.....	CVPHGWL.CDNQDDCGDG.....	SDEEGE.....	C	
075851	CGEGQMTCSGSH.....	CLPLALL.CDRQDDCGDG.....	TDEPSYP.....	C	
075851	CPQGLLACADGR.....	CLPPALL.CDGHPCDLA.....	ADEES.....	C	
075851	CVPGEVSCVDGT.....	CLGAIQL.CDGVWDCPDG.....	ADEGPGH.....	C	
ENSP00000262089						
= 075851	CGPFEFRCGSGE.....	CTPRGWR.CDQEEDCADG.....	SDERG.....	C	
ENSP00000262089						
	CAPHHAPCARGPH.....	CVSPEQL.CDGVRQCPDG.....	SDEGPDA.....	C	
075851	CPGLFPCGVAPGL.....	CLTPEQL.CDGI PDCPQG.....	EDEL D.....	C	
075851	CPEYTCPNGT.....	CIGFQLV.CDGQPDGCRPGQVGPSPPEEQG.....		C	
075851	CEPGVGLRCASGE.....	CVLRGGP.CDGVLDCEDEG.....	SDEEG.....	C	
ENSP00000262089						
	CGPGQTPCEVLG.....	CVEQAQV.CDGREDCLDG.....	SDERH.....	C	
075851	CSPSQLSCGSGE.....	CLSAERR.CDLRPDCQDG.....	SDEDEG.....	C	
C18ORF1	CKFTCTSGK.....	CLYLGSLVCNQNDGDN.....	SDEEN.....	C	
AAH07083/Q9NPF0						
	CPPTKFQCRTSGL.....	CVPLTWR.CDRDLDCSDG.....	SDEEE.....	C	
AAH07083/Q9NPF0						
	CLAGELRCTLSD.....	CIPLTWR.CDGHPCPDG.....	SDELG.....	C	
Q9HXB9	CSLGYFPCGNITK.....	CLPQLLH.CNGVDDCGNQ.....	ADEDN.....	C	
Q9BY79/Q96DQ9	CAHDEFRCQDLI.....	CLLPDSV.CDGFANCADG.....	SDET N.....	C	
Q9BY79/Q96DQ9	CGPSELSCQAGG.....	CKGVQWM.CDMWRDCTDG.....	SDDN.....	C	
BAB55257 =						
ENSP00000239367						
	CSRYHFFCDDGC.....	CIDITLA.CDGVQCCPDG.....	SDEDF.....	C	
095518 =	CPGEFLCSVNGL.....	CVPA.....	CDGVKDCPNG.....	LDERN.....	C
ENSP00000255793						
ENSP00000255793						
	CRATFQCKEDST.....	CISLPKV.CDGQPDCLNG.....	SDEEQ.....	C	
ENSP00000255793						
	CGTFTFQCEDRS.....	CVKKPNPQCDGRPDG.....	SDEEH.....	C	
Q8WXD0	C	QKGYFPCGNLTK	CLPRAFH	CDGKDDCGNG	ADEEN	C
Q8NBJO	C	STARYHCKNGL	CIDKSFI	CDGQNNCQDN	SDEES	C
Q8NBJO	C	GPTFFPCASGIH	CIIGRFR	CNGFEDCPDG	SDEEN	C
Q8NBJO	C	NIPGNFMCSNGR	CIPGAWQ	CDGLPDCFDK	SDEKE	C
MEGF7	C	ALDQFLCWNGR	CIGQRKL	CNGVNDGDN	SDESPQON	C
MEGF7	C	EEDFPCQNGY	CIRSLWH	CDGDNDGDN	SDEQ	C
MEGF7	C	RSGEFMCDSGL	CINAGWR	CDGDADCDQ	SDERN	C
MEGF7	C	TAEQFRCHSGR	CVRLSWR	CDGEDDCADN	SDEEN	C
MEGF7	C	SPLDFHCDNGK	CIRRSWV	CDGDNDGDN	SDEQD	C
MEGF7	C	NLEEFQCAAGR	CILDIYH	CDGDDDCGDW	SDESD	C
MEGF7	C	SDKEFRCSGDS	CIAEHWY	CDGDTCKDG	SDEEN	C
MEGF7	C	GRSHFTCAVSALGECT	CIPAQQW	CDGDNDGDN	SDEDEG	C
CAD61944	C	LQEEFQCLNHR	CVSAVQR	CDGVDACGDG	SDEAG	C

CAD61944	C	PPGHFPCGAAGTSGATA	CYLPADR CNYQTFCADG	ADERR	C
CAD61944	C	QPGNFRCRDEK	CVYETWV CDGQPD CADG	SDEWD	C
ENSG00000181006	C				
ENSP00000320248	C	PEITDFLCRDKK	CIASHLL CDYKPD CSDR	SDEAH	C
ENSP00000277547	C	NNRTFKCGNDI	CFRKQNAKCDGTVD CPDG	SDEEG	C
ENSP00000320022	C	PPGHHHCQNKV	CVEPQQL CDGEDN CGDL	SDENPLT	C
ENSP00000313222	C	KQGHLACGDL	CVPPEQL CDFEEQCAGG	EDEQA	C
	C	PGNSFSCGNSQ	CVTKVNPECDDQEDCSDG	SDEAH	C

Figure 11

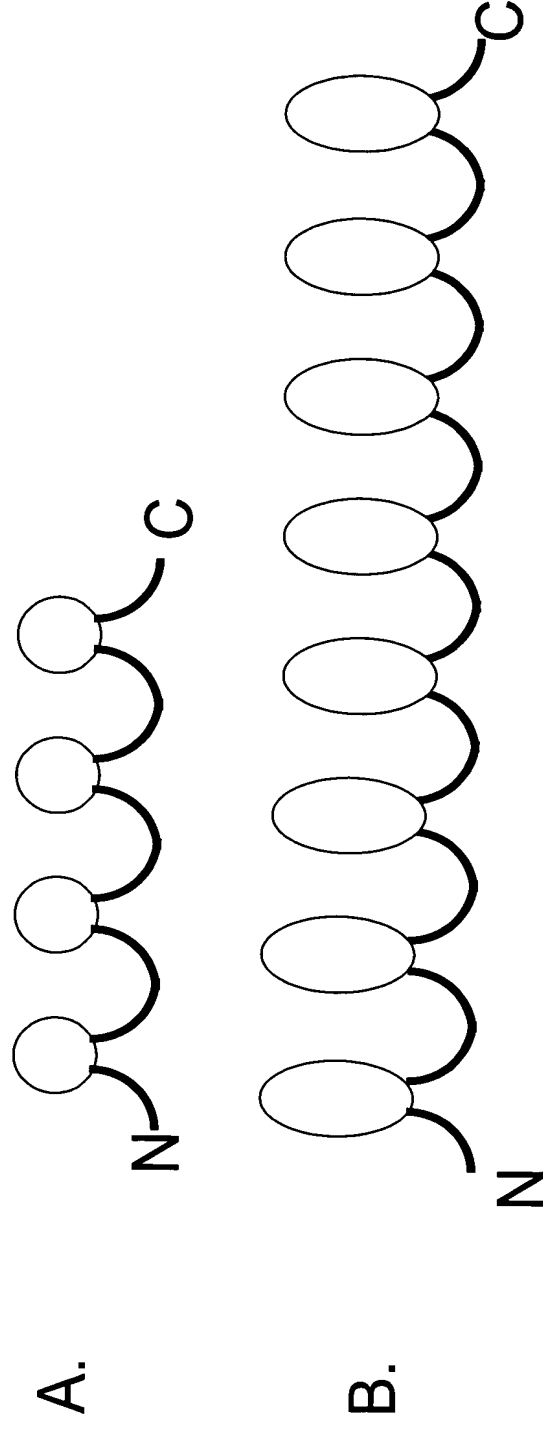
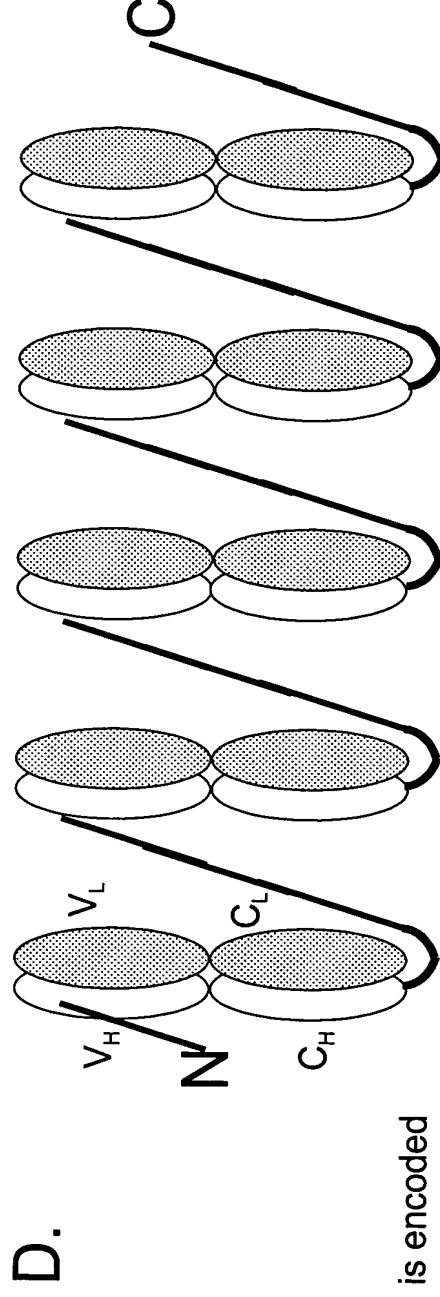
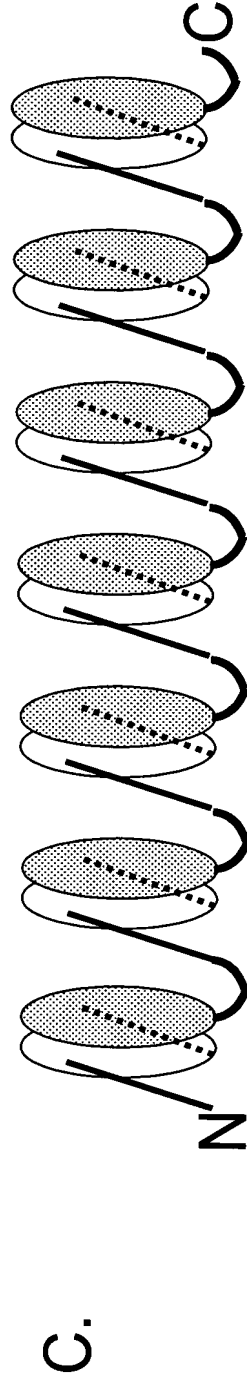


Figure 11



Light chain is encoded
as a separate protein

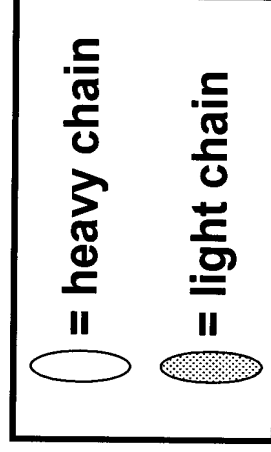
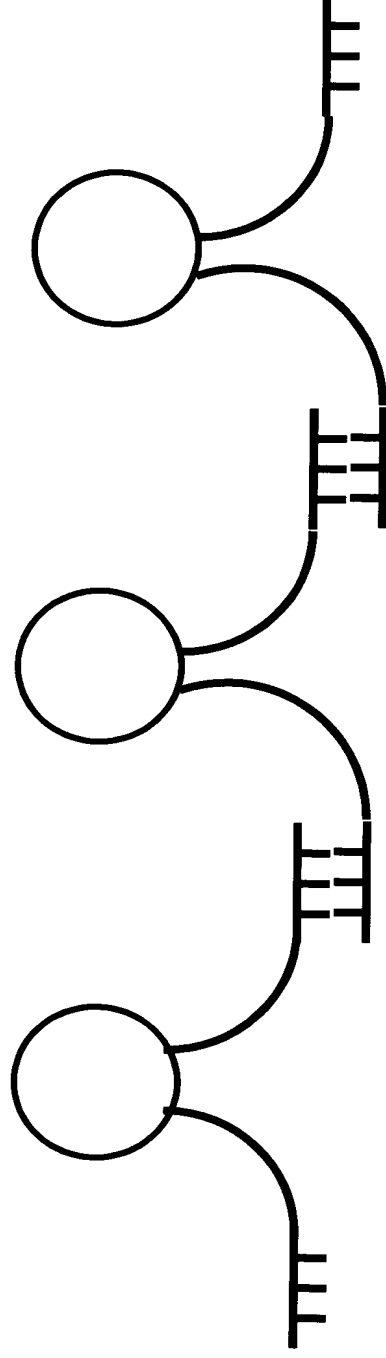


Figure 12

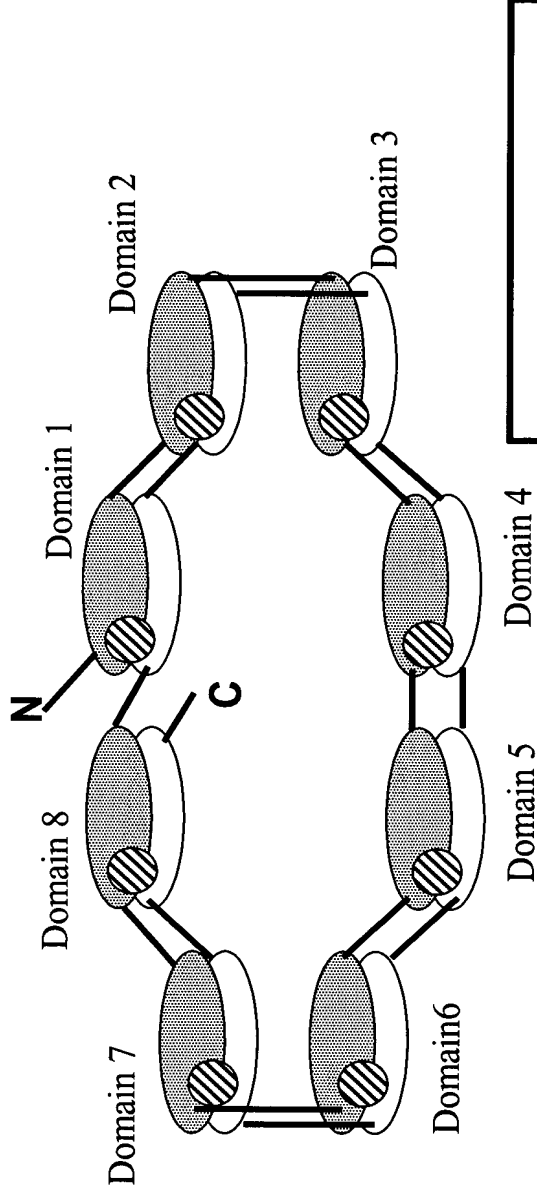


○ = any monomer domain
▄▄▄ = obligate heterodimeric linker

Figure 13

A.

One Chain
Multimer of
Fv's



B.

Two Chain
Multimer of
Fv's

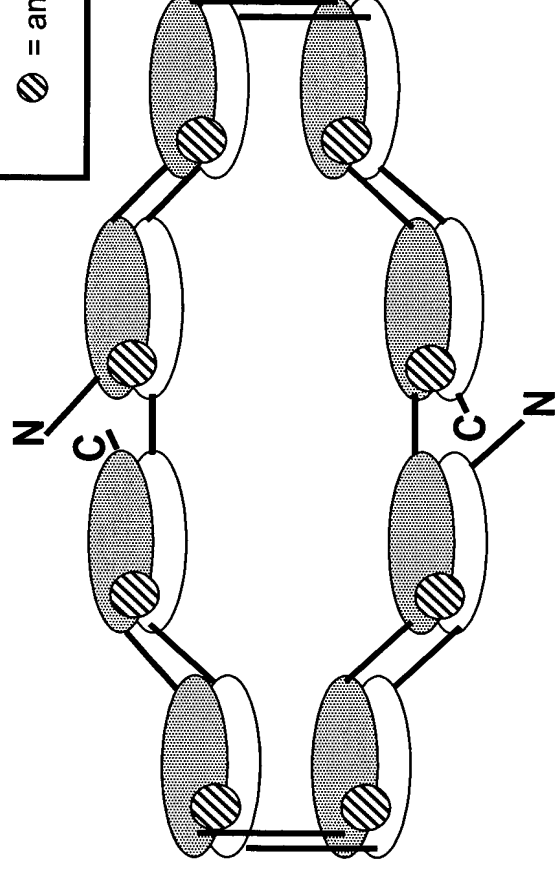


Figure 13C

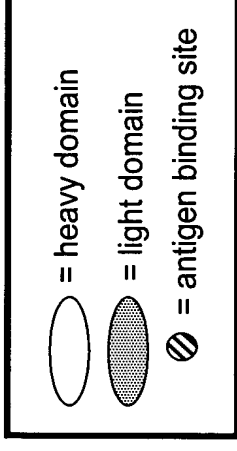
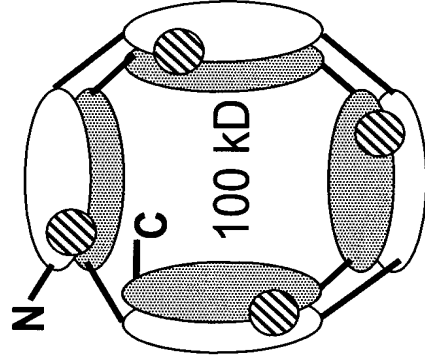


Figure 14

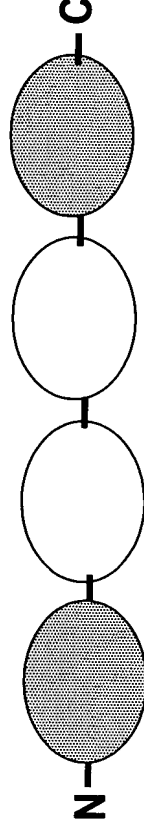
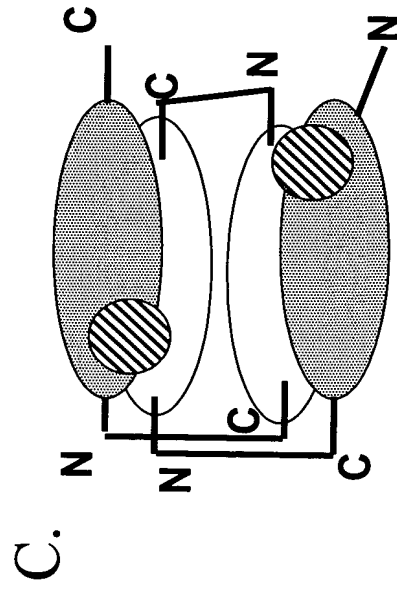
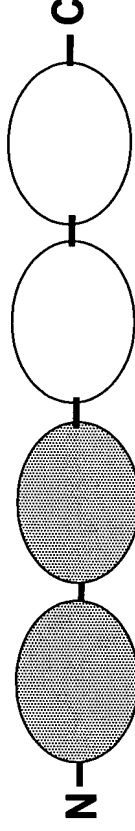
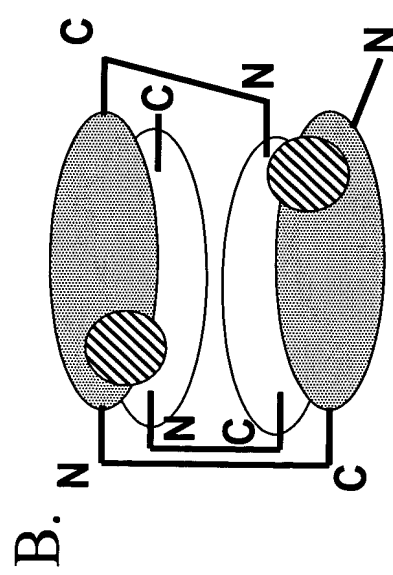
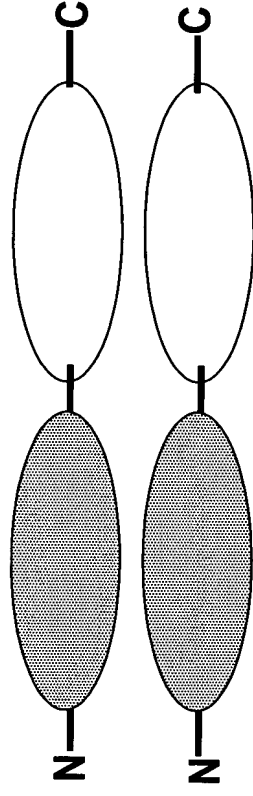
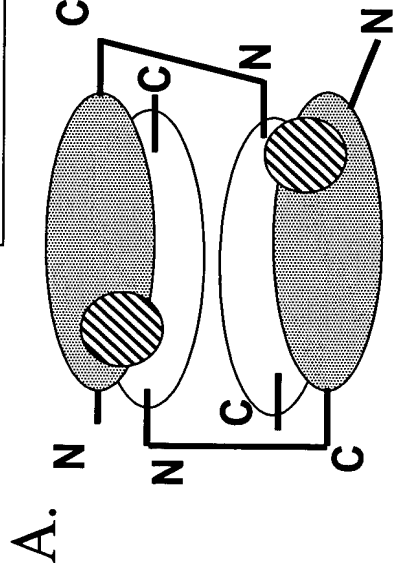


Figure 15

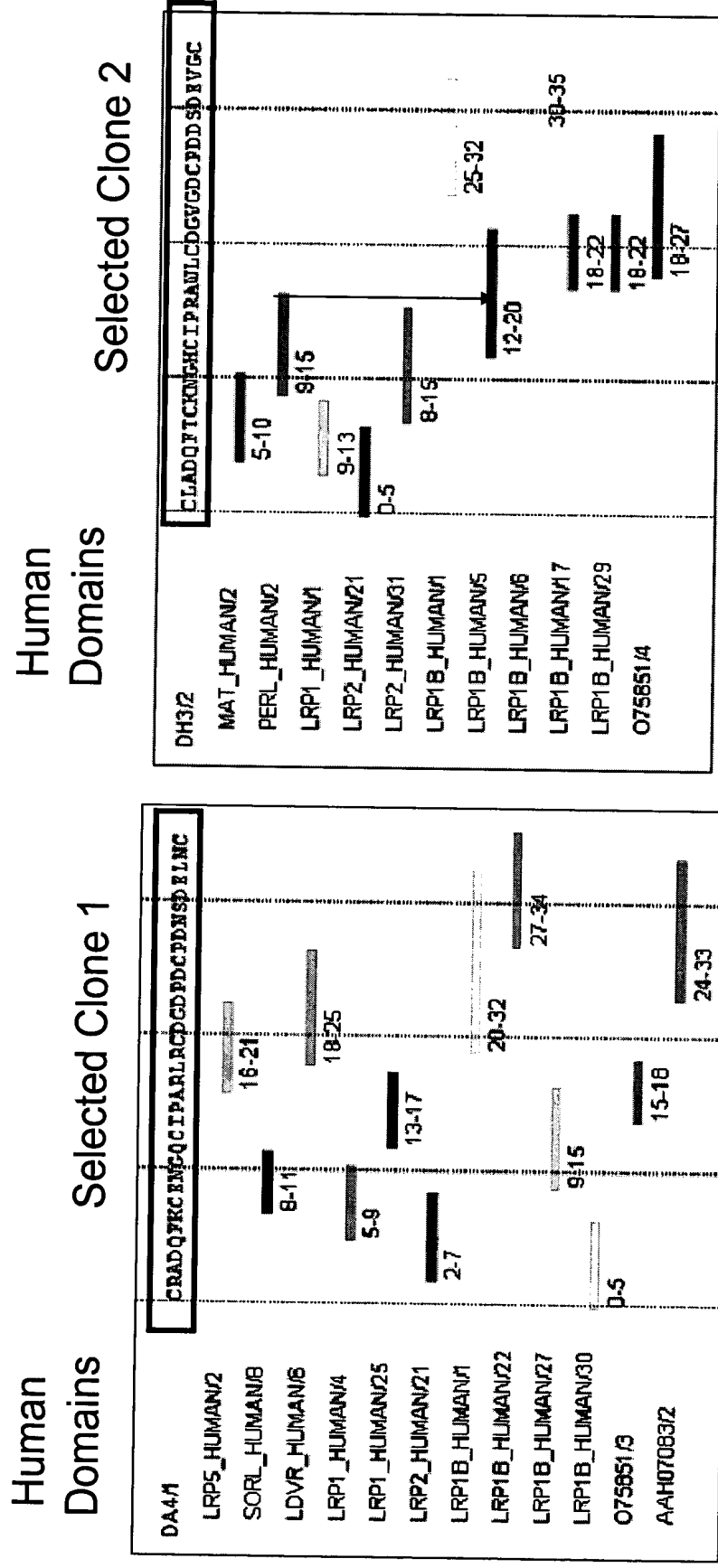


Figure 16
Cell Killing induced by Maxybodies

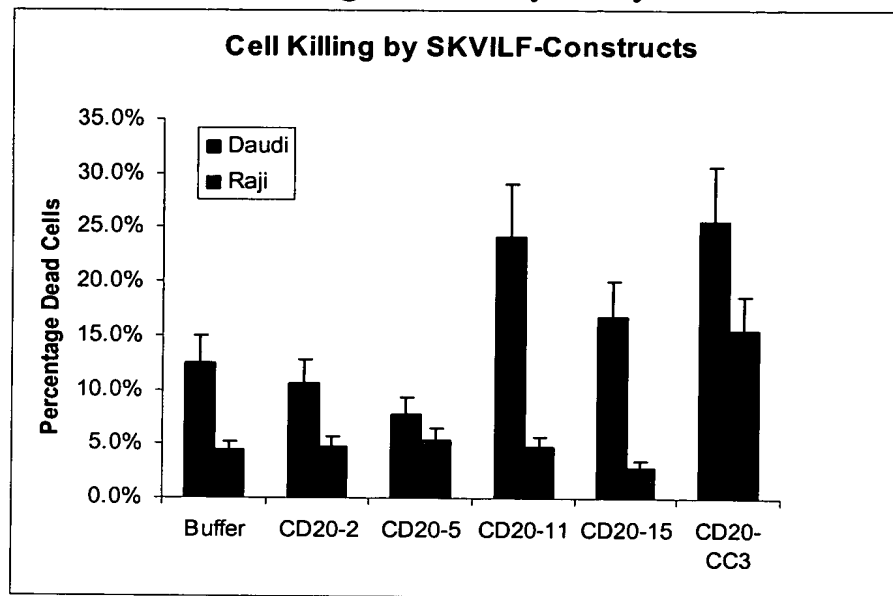


Figure 17: TPO-R Phage Specificity Data

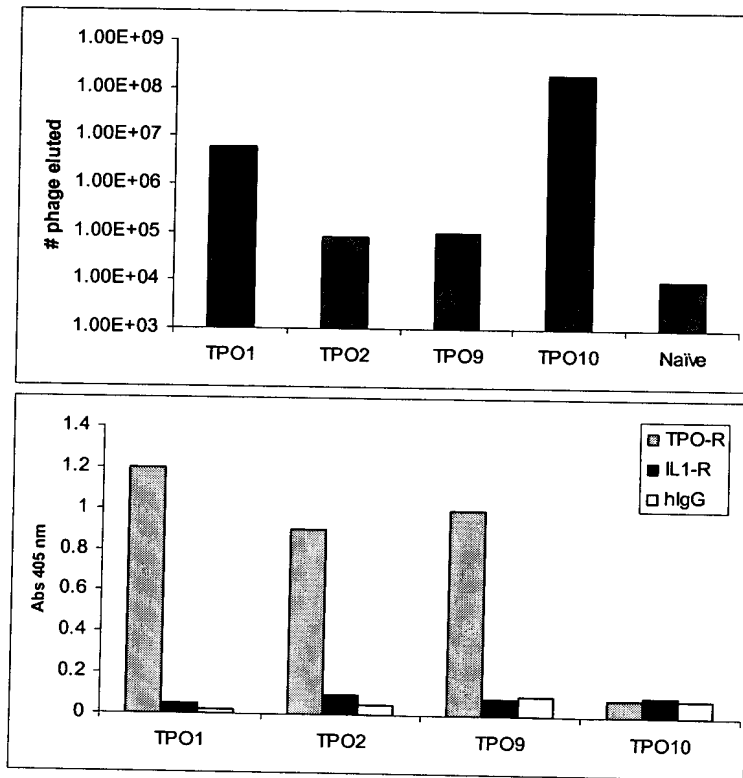


Figure 18: TF1 Proliferation Assay

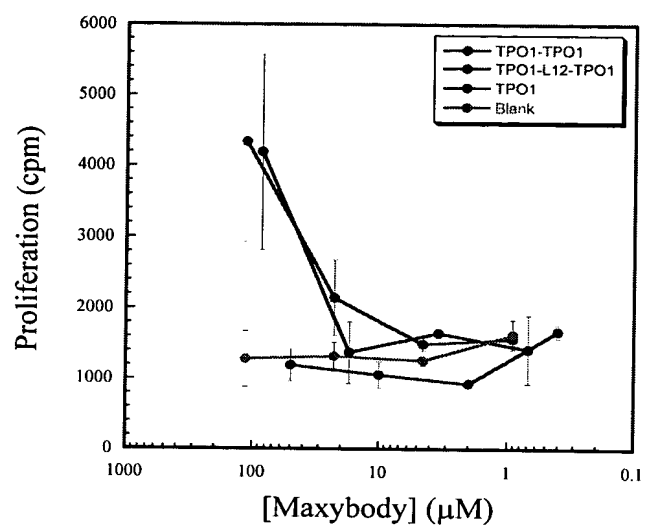


Figure 19 : Epitope mapping of IgE-Binding Monomer

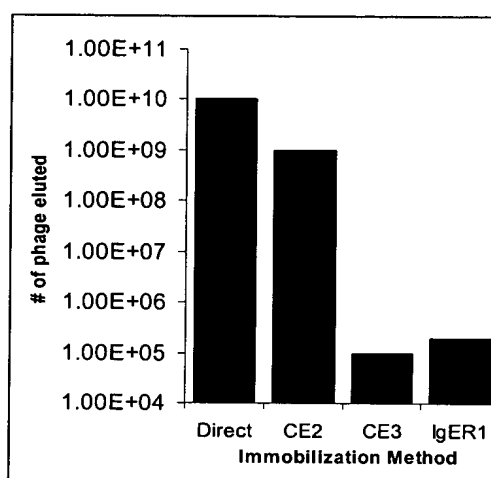


Figure 20

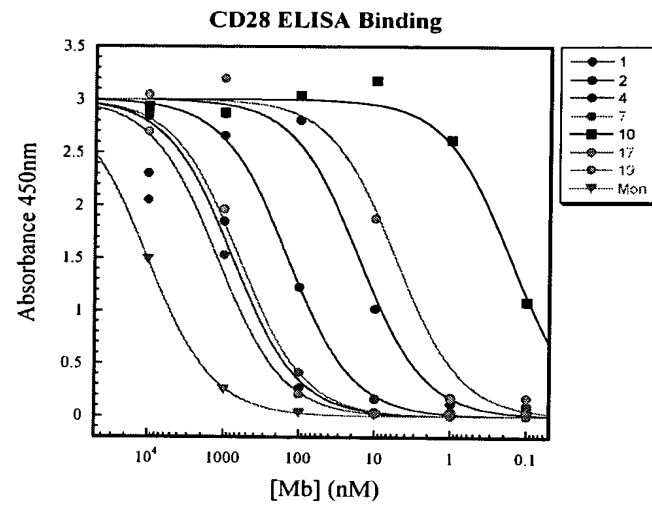


Figure 21

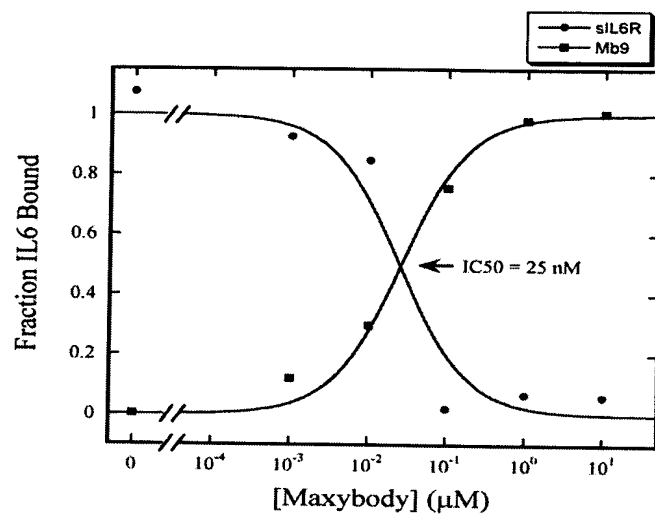


Figure 22

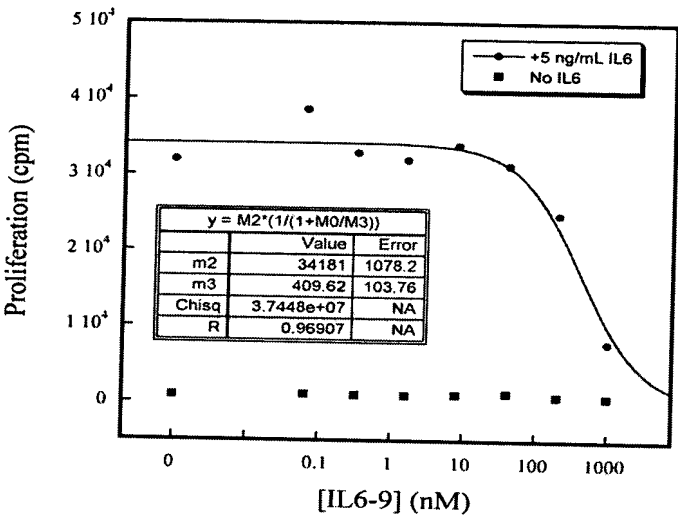


Figure 23

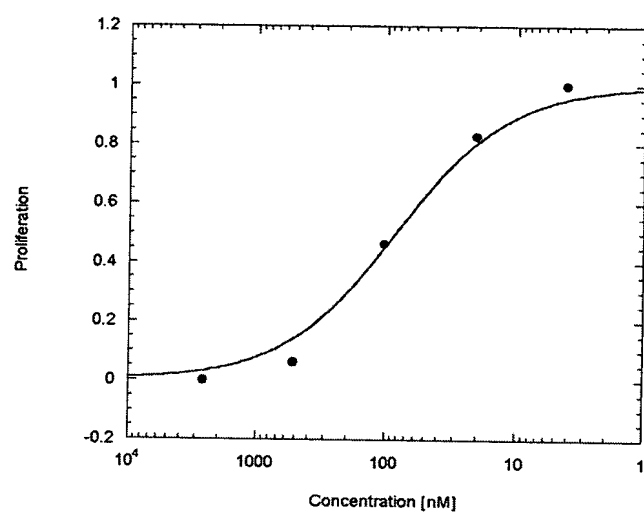
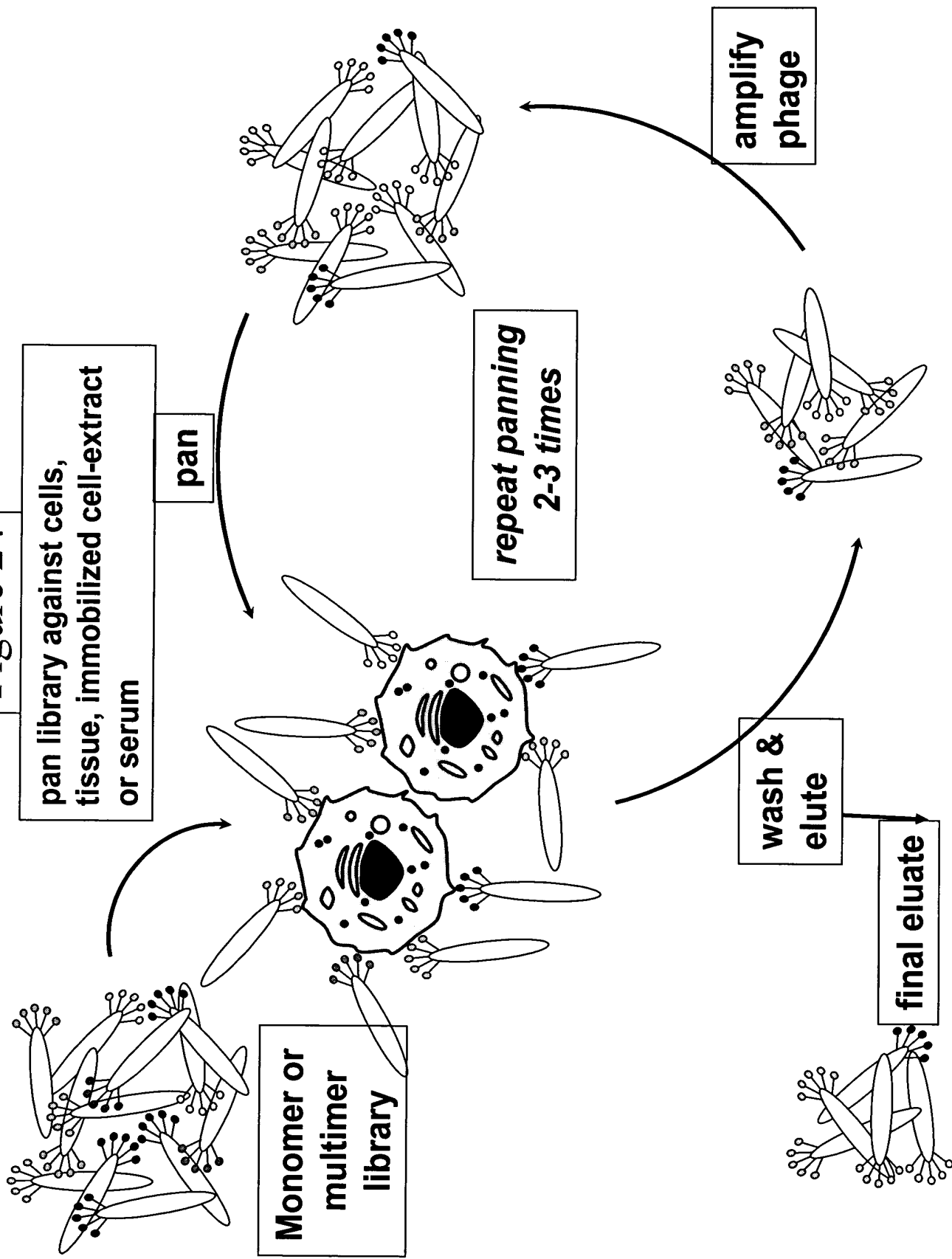


Figure 24



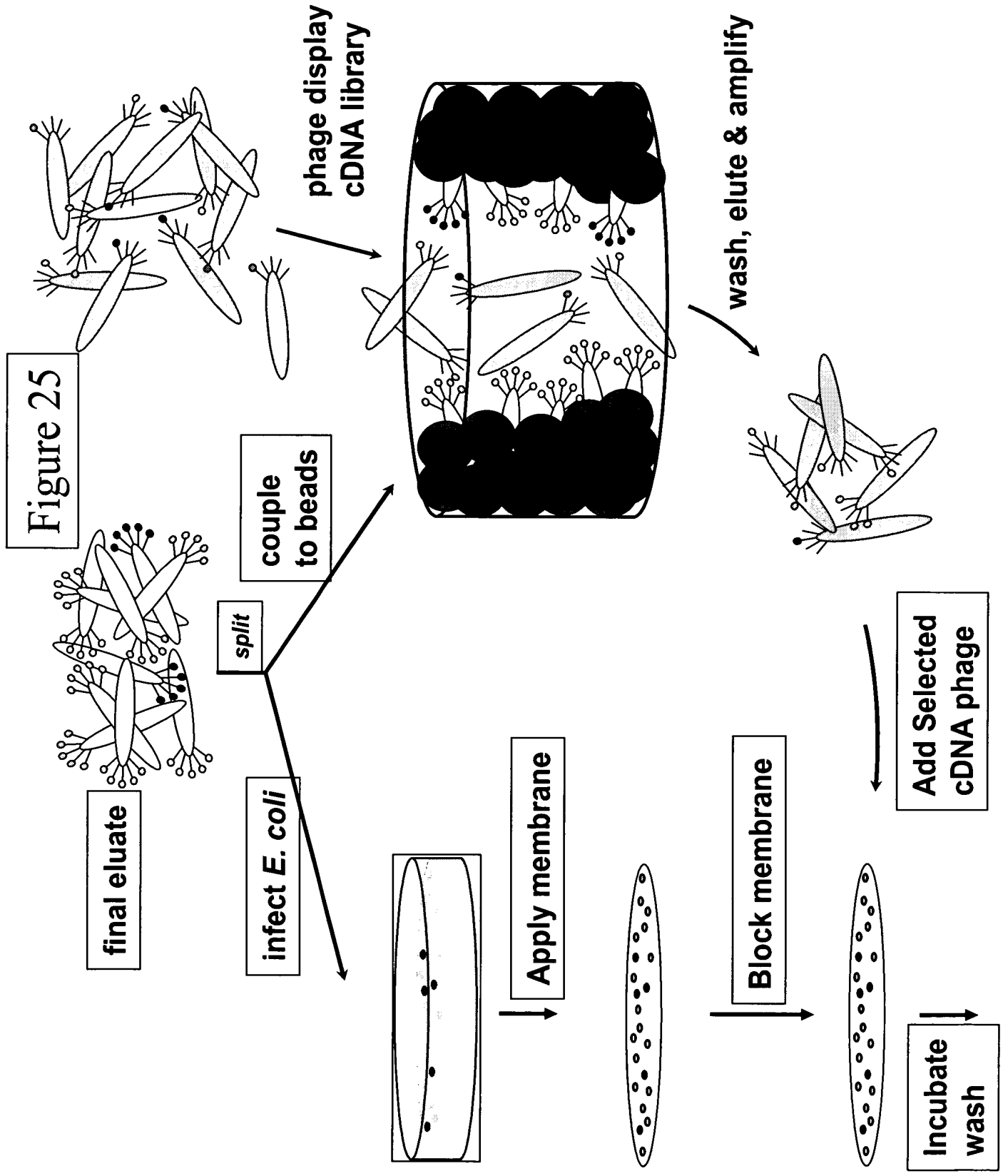
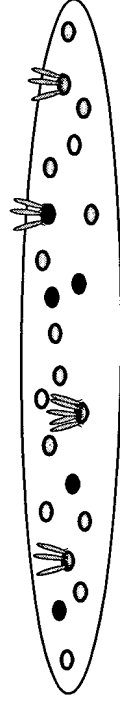
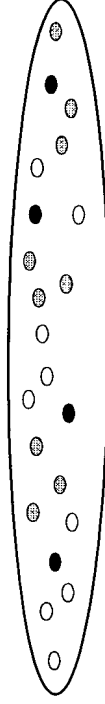


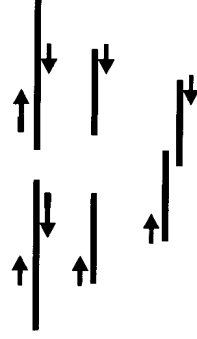
Figure 26



Stain membrane using cDNA phage specific MAb (HRP labeled)
Add substrate



Cut positive spots out of membrane and add to PCR tube
PCR amplify cDNA and MB sequences



Sequence PCR fragments

Figure 27

Format Variations

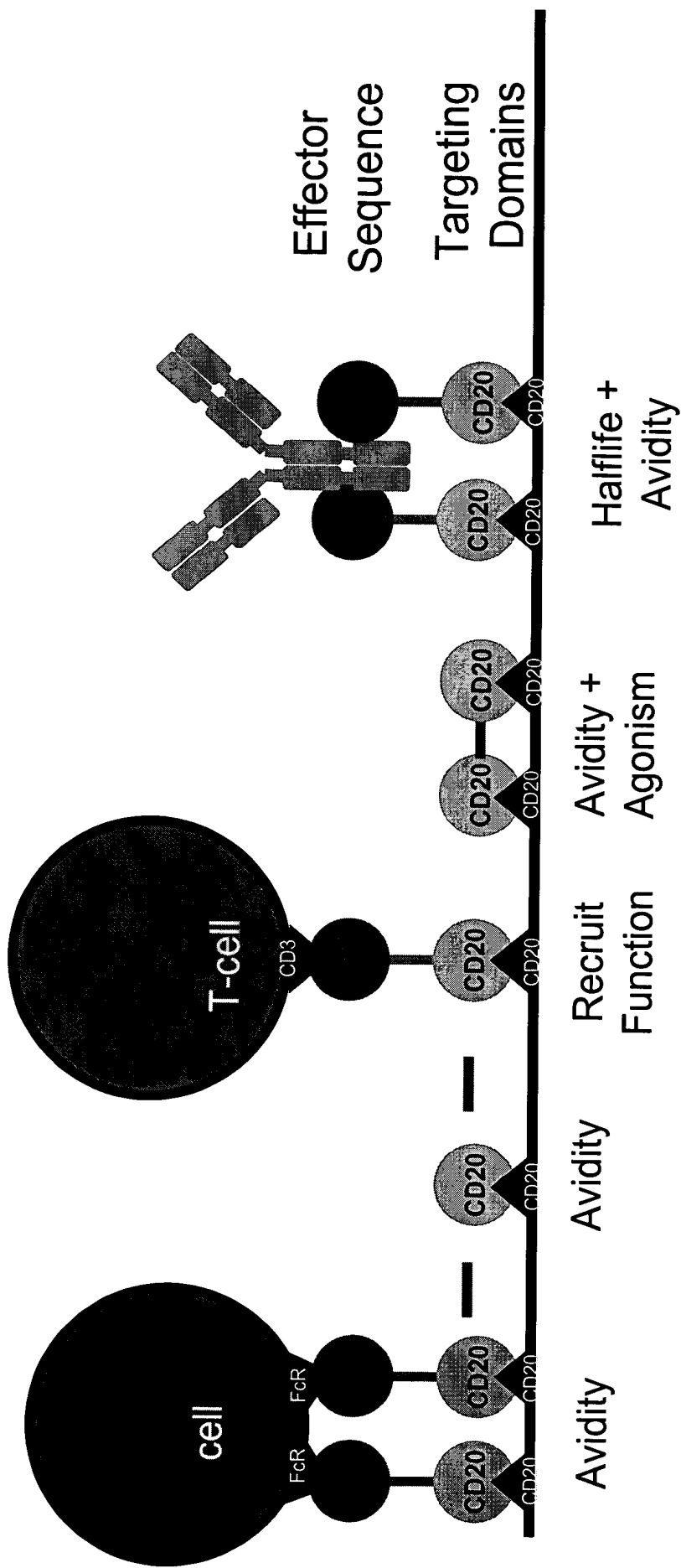
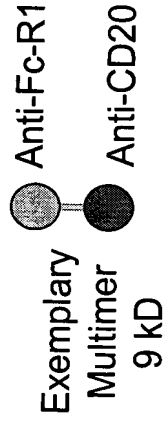


Figure 28

Multimer Format



Monovalent Binding

Complex Stabilization

